

Fig. 2

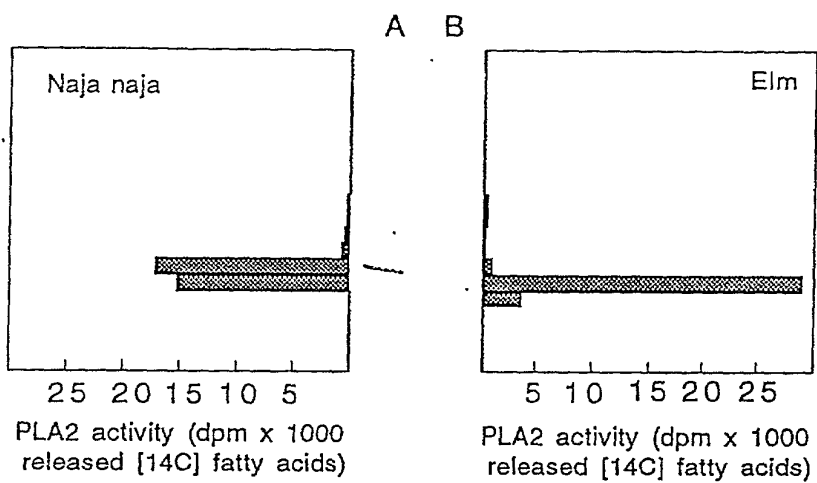


Fig. 3

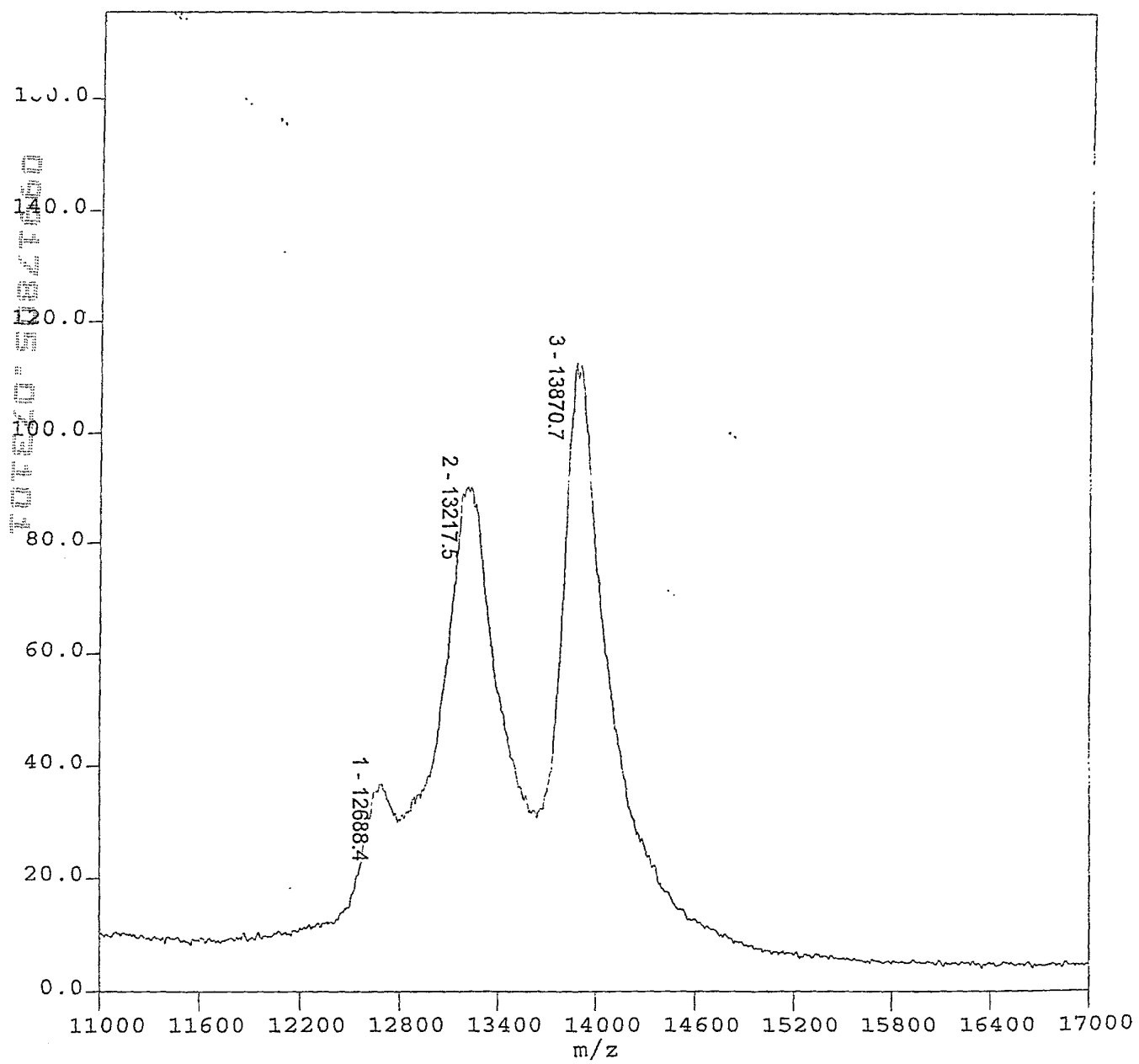


Fig. 4

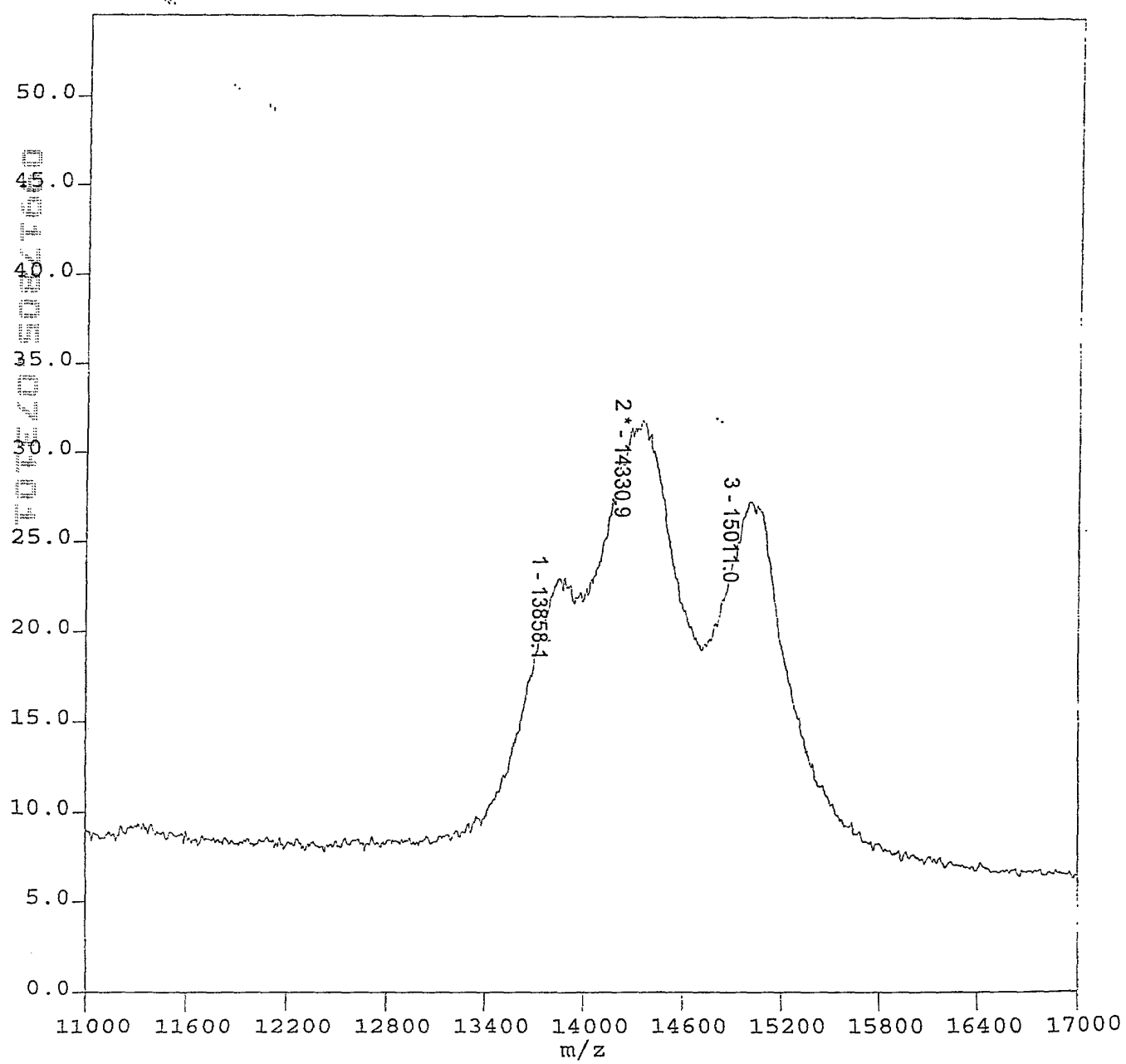


Fig. 5.

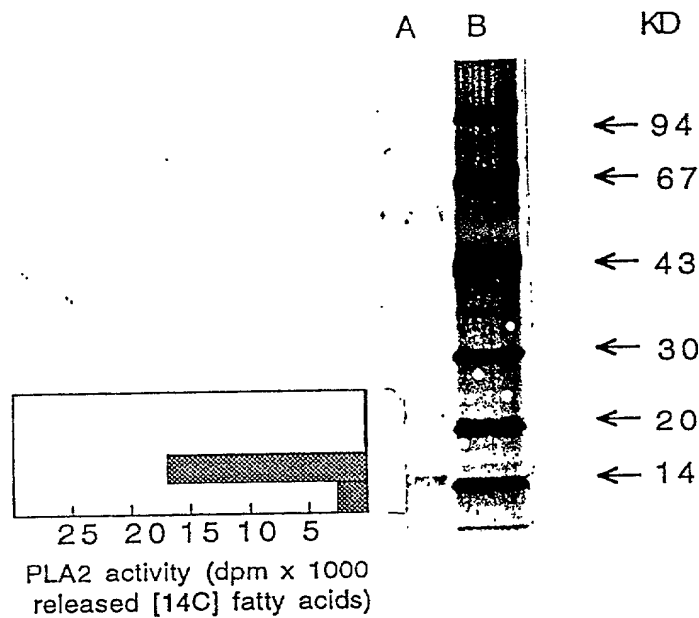


Fig. 6

D49050	MP--PRSHLL	A--LVFLA-A	GVLSA--TS	PPPPPCSRSC	AALNCDSVGI	43
D00035	MKFLVLAALL	T--VAAAE-G	GISPRA--VW	QFRNMIKCTI	PESDPLKDYN	45
D10070	MR-----TLW	I--MAVLL-V	GV-DGG--LW	QFENMIKV	KKSGILES-YS	38
M21054	MKLLVLAALL	T--VAAAD-S	GISPRA--VW	QFRMIKCVI	PGSDPFLEYN	45
X12605	MPAHLVLL	TVCVSLLEAS	SIPARPLNLY	QFGNMIQCAN	HGRRPTLAYA	50
X53406	MNPAHLVLL	AVCVSLLGAA	NVPPQHLNLY	QFKNMIVC--	AGTRPWIGYV	48
X53471	MR-----TLW	I--VAVCL-I	GV-EGS--LL	EFGMMILGE-	TGKNPLTSYS	38
X76289	MR-----TLW	I--MAVLL-V	GV-EGD--LW	QFGQMILKE-	TGKLPPFPYIT	38
Y00120	MRLLVLAALL	T--VGAGQ-A	GLNSRA--LW	QFNGMIKCKI	PSSEPLLDNFN	45
Y00377	MPAHLVLL	AVCVSLLGAS	AIPPLPLNLA	QFALVIKCAD	KGKRPWHYH	50

	Ca ²⁺ binding site				Active site										
D49050	RYG	YCG	GW	SG	CDGEE	PCD	DL	CC	RHD	HC	-VDK	KGLM	SVKC--HEKF	90	
D00035	DYG	YCG	LG	SG	---	TPMD	EL	CC	QTHD	HC	YSEAK	KLD	SCKFLLDNPNY	91	
D10070	AYG	YCG	AG	RG	---	KPKD	AT	DC	CFVHD	CC	YGV	TGCN	P-KL-GKITY	82	
M21054	NYG	YCG	LG	SG	---	TPMD	EL	CC	QTHD	NC	YDQ	AKLD	SCKFLLDNPNY	91	
X12605	DYG	YCG	AG	SG	---	TPMD	EL	DC	CCQAH	DC	YAG	K-K	GC-Y--PTL	91	
X53406	NYG	YCG	AG	SG	---	TPMD	EL	DC	CCVVD	NC	YEA	EKIP	GC-----NPK	89	
X53471	FYG	YCG	AG	KG	---	TPMD	AT	DC	CFVHD	CC	YGN	---	LP	DC-----SPK	76
X76289	TYG	YCG	AG	QG	---	QPKD	AT	DC	CFVHD	CC	Y	---	KLT	NC-----KPK	76
Y00120	NYG	YCG	LG	SG	---	TPMD	DL	DC	CCQTHD	NC	Y	KQAK	KLD	SCKVLVDNPNY	91
Y00377	DYG	YCG	FG	SG	---	TPMD	EL	DC	CCCKTHD	CC	Y	QA	EK-K	GC-----YPK	90

Fig. 6 cont.

D49050	KNCMRKVKKA	GKIGFSRK--	CPYEMAMAT	MTSGMDMAIM	-----LS-Q	130
D00035	TKIYSYSCSG	SEITCSSKNK	DCQAFICNCD	RSAAICFSKA	-----PY-N	134
D10070	SWNNGDIVCE	GDGPCKEVC-	ECDRAAAICF	RDNLDTYDRN	-----KYWR	125
M21054	THTYSYSCSG	SAITCSSKNK	ECFAFICNCD	RNAAICFSKA	-----PY-N	134
X12605	T-LYSWQCIE	KTPTCNSKT-	GCERSVDCDC	ATAAKCFACA	-----PY-N	132
X53406	TKTYSYTCTK	PNLTCTDAAG	TCARRIVDCDC	RTAAICFAAA	-----PY-N	132
X53471	TDRYKYHREN	GAIVCGKGT-	SCENRICECD	RAAAICFRKN	LKTYNYIYRN	125
X76289	TDRYSYSREN	GVIICGEGT-	FCEKQICECD	KAAAVCFREN	LRTYKKRYMA	125
Y00120	TNNYSYSCSN	NEITCSSENN	ACEAFICNCD	RNAAICFSKV	-----PY-N	134
Y00377	LTMYSYCGG	DGPYCNST-	ECQRFVDCDC	VRAADCFAFY	-----PY-N	132

D49050	LGTKLEL
D00035	KEHKNLDTKKYC
D10070	YPASNCQEDSEPC
M21054	KAHKNLDTKKYCQS
X12605	KKNYNIDTEKRCQ
X53406	TNNFMISSTHCQ
X53471	YPDFLCKKESEKC
X76289	YPDVLCCKPAEKC
Y00120	KEHKNLDTKKYC
Y00377	NKNYNINTSKRCK

1	16	31
N-terminal-----	-----XN/GVQ	ATGTSISVGKCCRRK
D47724	MRFFLKLAAPRCVLLL	LLGVTPAKDQCCSRT
D47653	MRFFLKLAAPRCVLLL	LLGVTPAKDQCCSRT
D49050	-----MPPRSPLLAL	SATSPPPP--CRRS

Fig. 7

46	61	76	30	83	88	76
CXXXFCYGP	KYCGILYSGCPGERP	CDALDXCC				
CESQFCTIAPLLRYG	KYCGILYSGCPGERP	CDGXDXCMVHDH				
CESQFCTIAPLLRYG	KYCGVGVSGCDGEFP	CDDLDAACCRDHDHCV				
CAALNCDSVG-IRYG						

Ca²⁺-binding site active site